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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/075,446

DATE: 04/24/2002
 TIME: 10:12:39

Input Set : N:\Crf3\RULE60\10075446.raw
 Output Set: N:\CRF3\04242002\J075446.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: RUBEN, STEVEN M.
 6 JIMENEZ, PABLO
 7 DUAN, D. ROXANNE
 8 RAMPY, MARK A.
 9 MENDRICK, DONNA
 10 ZHANG, JUN
 11 NI, JIAN
 12 MOORE, PAUL A.
 13 COLEMAN, TIMOTHY A.
 14 GRUBER, JOACHIM R.
 W--> 15 DILLON, PATRICK J.
 W--> 16 GENTZ, REINER L.

ENTERED

(ii) TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

(iii) NUMBER OF SEQUENCES: 148

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 (B) STREET: 1100 NEW YORK AVE, NW, SUITE 600
 (C) CITY: WASHINGTON
 (D) STATE: DC
 (E) COUNTRY: USA
 (F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/075,446
 (B) FILING DATE: 15-Feb-2002

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/023,082
 (B) FILING DATE:
 (A) APPLICATION NUMBER: PCT/US95/01790
 (B) FILING DATE: 14-FEB-1995
 (A) APPLICATION NUMBER: US 08/461,195
 (B) FILING DATE: 05-JUN-1995
 (A) APPLICATION NUMBER: US 60/023,852
 (B) FILING DATE: 13-AUG-1996
 (A) APPLICATION NUMBER: US 60/039,045
 (B) FILING DATE: 28-FEB-1997

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63 (A) APPLICATION NUMBER: US 08/862,432
 64 (B) FILING DATE: 23-MAY-1997
 67 (A) APPLICATION NUMBER: US 08/910,875
 68 (B) FILING DATE: 13-AUG-1997
 71 (A) APPLICATION NUMBER: US 60/055,561
 72 (B) FILING DATE: 13-AUG-1997
 74 (viii) ATTORNEY/AGENT INFORMATION:
 75 (A) NAME: STEFFFE, ERIC K.
 76 (B) REGISTRATION NUMBER: 36,688
 77 (C) REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
 79 (ix) TELECOMMUNICATION INFORMATION:
 80 (A) TELEPHONE: 202-371-2600
 81 (B) TELEFAX: 202-371-2540
 83 (2) INFORMATION FOR SEQ ID NO: 1:
 85 (i) SEQUENCE CHARACTERISTICS:
 86 (A) LENGTH: 627 base pairs
 87 (B) TYPE: nucleic acid
 88 (C) STRANDEDNESS: double
 89 (D) TOPOLOGY: both
 91 (ii) MOLECULE TYPE: DNA (genomic)
 94 (ix) FEATURE:
 95 (A) NAME/KEY: CDS
 96 (B) LOCATION: 1..624
 99 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 101 ATG TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG 48
 102 Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
 103 1 5 10 15
 105 CCC GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC 96
 106 Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
 107 20 25 30
 109 GTC CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG 144
 110 Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
 111 35 40 45
 113 GCC ACC AAC TCT TCT TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA 192
 114 Ala Thr Asn Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
 115 50 55 60
 117 AGG CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA 240
 118 Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 119 65 70 75 80
 121 AAG CTA TTC TCT ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG 288
 122 Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
 123 85 90 95
 125 AAG GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG 336
 126 Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
 127 100 105 110
 129 ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC 384
 130 Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
 131 115 120 125
 133 AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA 432

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Input Set : N:\Crf3\RULE60\10075446.raw
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134	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	
135	130						135					140					
137	GAA	TTT	AAC	AAT	GAC	TGT	AAG	CTG	AAG	GAG	AGG	ATA	GAG	GAA	AAT	GGA	480
138	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	
139	145						150			155		160					
141	TAC	AAT	ACC	TAT	GCA	TCA	TTT	AAC	TGG	CAG	CAT	AAT	GGG	AGG	CAA	ATG	528
142	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	
143							165			170		175					
145	TAT	GTG	GCA	TTG	AAT	GGA	AAA	GGA	GCT	CCA	AGG	AGA	GGA	CAG	AAA	ACA	576
146	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	
147							180			185		190					
149	CGA	AGG	AAA	AAC	ACC	TCT	GCT	CAC	TTT	CTT	CCA	ATG	GTG	GTA	CAC	TCA	624
150	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	Val	His	
151							195			200		205					
153	TAG																627
156	(2)	INFORMATION	FOR	SEQ	ID	NO:	2:										
158		(i)	SEQUENCE	CHARACTERISTICS:													
159			(A)	LENGTH:	208	amino	acids										
160			(B)	TYPE:	amino	acid											
161			(D)	TOPOLOGY:	linear												
163		(ii)	MOLECULE	TYPE:	protein												
165		(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	2:									
167	Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu	
168	1				5					10				15			
170	Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Val	Ser	Ser	
171									20			25		30			
173	Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	
174							35			40		45					
176	Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	
177							50			55		60					
179	Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	
180							65			70		75				80	
182	Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	
183							85			90			95				
185	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	
186							100			105			110				
188	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	
189							115			120			125				
191	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	
192							130			135			140				
194	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	
195							145			150			155			160	
197	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	
198							165			170			175				
200	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	
201							180			185			190				
203	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser	
204							195			200			205				
207	(2)	INFORMATION	FOR	SEQ	ID	NO:	3:										

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Input Set : N:\Crf3\RULE60\10075446.raw
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209	(i) SEQUENCE CHARACTERISTICS:	
210	(A) LENGTH: 36 base pairs	
211	(B) TYPE: nucleic acid	
212	(C) STRANDEDNESS: single	
213	(D) TOPOLOGY: linear	
215	(ii) MOLECULE TYPE: cDNA	
220	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
222	CCCCACATGT GGAAATGGAT ACTGACACAT TGTGCC	36
224	(2) INFORMATION FOR SEQ ID NO: 4:	
226	(i) SEQUENCE CHARACTERISTICS:	
227	(A) LENGTH: 35 base pairs	
228	(B) TYPE: nucleic acid	
229	(C) STRANDEDNESS: single	
230	(D) TOPOLOGY: linear	
232	(ii) MOLECULE TYPE: cDNA	
237	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
239	CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG	35
241	(2) INFORMATION FOR SEQ ID NO: 5:	
243	(i) SEQUENCE CHARACTERISTICS:	
244	(A) LENGTH: 36 base pairs	
245	(B) TYPE: nucleic acid	
246	(C) STRANDEDNESS: single	
247	(D) TOPOLOGY: linear	
249	(ii) MOLECULE TYPE: cDNA	
254	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
256	CATGCCATGG CGTGCCAAGC CCTTGGTCAG GACATG	36
258	(2) INFORMATION FOR SEQ ID NO: 6:	
260	(i) SEQUENCE CHARACTERISTICS:	
261	(A) LENGTH: 35 base pairs	
262	(B) TYPE: nucleic acid	
263	(C) STRANDEDNESS: single	
264	(D) TOPOLOGY: linear	
266	(ii) MOLECULE TYPE: cDNA	
271	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
273	CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG	35
275	(2) INFORMATION FOR SEQ ID NO: 7:	
277	(i) SEQUENCE CHARACTERISTICS:	
278	(A) LENGTH: 35 base pairs	
279	(B) TYPE: nucleic acid	
280	(C) STRANDEDNESS: single	
281	(D) TOPOLOGY: linear	
283	(ii) MOLECULE TYPE: cDNA	
288	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
290	GCGGGATCCG CCATCATGTG GAAATGGATA CTCAC	35
292	(2) INFORMATION FOR SEQ ID NO: 8:	
294	(i) SEQUENCE CHARACTERISTICS:	
295	(A) LENGTH: 27 base pairs	
296	(B) TYPE: nucleic acid	
297	(C) STRANDEDNESS: single	

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298	(D) TOPOLOGY: linear	
300	(ii) MOLECULE TYPE: cDNA	
305	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
307	GCGCGGTACC ACAAACGTTG CCTTCCT	27
309	(2) INFORMATION FOR SEQ ID NO: 9:	
311	(i) SEQUENCE CHARACTERISTICS:	
312	(A) LENGTH: 40 base pairs	
313	(B) TYPE: nucleic acid	
314	(C) STRANDEDNESS: single	
315	(D) TOPOLOGY: linear	
317	(ii) MOLECULE TYPE: cDNA	
322	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
324	TAACGAGGAT CCGCCATCAT GTGGAAATGG ATACTGACAC	40
326	(2) INFORMATION FOR SEQ ID NO: 10:	
328	(i) SEQUENCE CHARACTERISTICS:	
329	(A) LENGTH: 38 base pairs	
330	(B) TYPE: nucleic acid	
331	(C) STRANDEDNESS: single	
332	(D) TOPOLOGY: linear	
334	(ii) MOLECULE TYPE: cDNA	
339	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
341	TAAGCACTCG AGTGAGTGTG CCACCATTTG AAGAAATG	38
343	(2) INFORMATION FOR SEQ ID NO: 11:	
345	(i) SEQUENCE CHARACTERISTICS:	
346	(A) LENGTH: 54 base pairs	
347	(B) TYPE: nucleic acid	
348	(C) STRANDEDNESS: single	
349	(D) TOPOLOGY: linear	
351	(ii) MOLECULE TYPE: cDNA	
356	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
358	ATTAACCCTC ACTAAAGGGA GGCCATGTGG AAATGGATAC TGACACATTG TGCC	54
360	(2) INFORMATION FOR SEQ ID NO: 12:	
362	(i) SEQUENCE CHARACTERISTICS:	
363	(A) LENGTH: 35 base pairs	
364	(B) TYPE: nucleic acid	
365	(C) STRANDEDNESS: single	
366	(D) TOPOLOGY: linear	
368	(ii) MOLECULE TYPE: cDNA	
373	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
375	CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG	35
377	(2) INFORMATION FOR SEQ ID NO: 13:	
379	(i) SEQUENCE CHARACTERISTICS:	
380	(A) LENGTH: 206 amino acids	
381	(B) TYPE: amino acid	
382	(C) STRANDEDNESS: Not Relevant	
W--> 383	(D) TOPOLOGY: Not Relevant	
385	(ii) MOLECULE TYPE: protein	
390	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
392	Met Ser Gly Pro Gly Thr Ala Ala Val Ala Leu Pro Ala Val Leu	

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/075,446

DATE: 04/24/2002
TIME: 10:12:40

Input Set : N:\Crf3\RULE60\10075446.raw
Output Set: N:\CRF3\04242002\J075446.raw

L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:15 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:16 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:383 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:437 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:491 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:557 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:602 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:647 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:702 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:756 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:811 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:871 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:1183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:1225 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:1246 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:2619 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:2623 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:2627 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
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L:2635 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:2639 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:2643 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:3250 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=96
L:3573 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=112
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L:3797 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=120
L:3906 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=124
L:4015 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=128
L:4124 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=132
L:4233 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=136
L:4342 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=140
L:4483 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=146